40 45 50

Gly Arg Val Lys Tyr Gly Leu His Asn Leu Gln Ile Ser
55 60 65

His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Asp
70 75

Ala Lys Thr Ile Asp Val Ala Ile Gln Asn Val Ser Val
80 85 90

Val Phe Lys Gly Thr Leu Asn Tyr Ser Tyr Thr Ser Ala
95 100

Trp Gly Leu Gly Ile Asn Gln Ser Val Asp Phe Glu Ile
105 110 115

Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Glu Leu Thr
120 125 130

Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp Cys
135 140

Tyr Leu Ala Phe His Lys Leu Leu Leu His Leu Gln Gly
145 150 155

Glu Arg Glu Pro Gly Trp Leu Lys Gln Leu Phe Thr Asn
160 165

Phe Ile Ser Phe Thr Leu Lys Leu Ile Leu Lys Arg Gln
170 175 180

Val Cys Asn Glu Ile Asn Thr Ile Ser Asn Ile Met Ala
185 190 195

Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
200 205

Gly Asp Ile Gly Val Asp Ile Ser Val Thr Gly Ala Pro
210 215 220

Val Ile Thr Ala Thr Tyr Leu Glu Ser His His Lys Gly
225 230

His Phe Thr His Lys Asn Val Ser Glu Ala Phe Pro Leu
235 240 245

Arg Ala Phe Pro Pro Gly Leu Leu Gly Asp Ser Arg Met
250 255 260

Leu Tyr Phe Trp Phe Ser Asp Gln Val Leu Asn Ser Leu
265 270

Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser
275 280 285

Leu Thr Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln

290 295

Gly Phe Asp Thr Asn Gln Glu Ile Phe Gln Glu Leu Ser
300 305 310

Arg Gly Leu Pro Thr Gly Gln Ala Gln Val Ala Val His
315 320 325

Cys Leu Lys Val Pro Lys Ile Ser Cys Gln Asn Arg Gly
330 335

Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe
340 345 350

Pro Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe
355 360

Glu Glu Asp Ile Ile Thr Thr Val Gln Ala Ser Tyr Ser
365 370 375

Gln Lys Lys Leu Phe Leu His Leu Leu Asp Phe Gln Cys
380 385 390

Val Pro Ala Ser Gly Arg Ala Gly Ser Ser Ala Asn Leu
395 400

Ser Val Ala Leu Arg Thr Glu Ala Lys Ala Val Ser Asn
405 410 415

Leu Thr Glu Ser Arg Ser Glu Ser Leu Gln Ser Ser Leu
420 425

Arg Ser Leu Ile Ala Thr Val Gly Ile Pro Glu Val Met
430 435 440

Ser Arg Leu Glu Val Ala Phe Thr Ala Leu Met Asn Ser
445 450 455

Lys Gly Leu Asp Leu Phe Glu Ile Ile Asn Pro Glu Ile
460 465

Ile Thr Leu Asp Gly Cys Leu Leu Leu Gln Met Asp Phe
470 475 480

Gly Phe Pro Lys His Leu Leu Val Asp Phe Leu Gln Ser
485 490

Leu Ser
495

(2) INFORMATION FOR SEQ ID NO: 3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1428 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE:
(A) NAME: Structural coding sequence for mature human CETP
(B) LOCATION:
(x) PUBLICATION INFORMATION:
(A) AUTHORS: Drayna, Dennis, et al.
(B) TITLE: Cloning and sequencing of human cholesteryl ester transfer cDNA
(C) JOURNAL: Nature
(D) VOLUME: 327
(E) ISSUE:
(F) PAGES: 632 - 634
(G) DATE: 18-JUN-1987
(K) RELEVANT RESIDUES IN SEQ ID NO:3: FROM 1 TO 1428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGCTCCAAAG GCACCTCGCA CGAGGCAGGC ATCGTGTGCC GCATCACCAA 50

GCCTGCCCTC CTGGTGTTGA ACCACGAGAC TGCCAAGGTG ATCCAGACCG 100

CCTTCCAGCG AGCCAGCTAC CCAGATATCA CGGGCGAGAA GGCCATGATG 150

CTCCTTGGCC AAGTCAAGTA TGGGTTGCAC AACATCCAGA TCAGCCACTT 200

GTCCATCGCC AGCAGCCAGG TGGAGCTGGT GGAAGCCAAG TCCATTGATG 250

TCTCCATTCA GAACGTGTCT GTGGTCTTCA AGGGGACCCT GAAGTATGGC 300

TACACCACTG CCTGGTGGCT GGGTATTGAT CAGTCCATTG ACTTCGAGAT 350

CGACTCTGCC ATTGACCTCC AGATCAACAC ACAGCTGACC TGTGACTCTG 400

GTAGAGTGCG GACCGATGCC CCTGACTGCT ACCTGTCTTT CCATAAGCTG 450

CTCCTGCATC TCCAAGGGGA GCGAGAGCCT GGGTGGATCA AGCAGCTGTT 500

CACAAATTTC ATCTCCTTCA CCCTGAAGCT GGTCCTGAAG GGACAGATCT 550

GCAAAGAGAT CAACGTCATC TCTAACATCA TGGCCGATTT TGTCCAGACA 600

AGGGCTGCCA GCATCCTTTC AGATGGAGAC ATTGGGGTGG ACATTTCCCT 650

GACAGGTGAT CCCGTCATCA CAGCCTCCTA CCTGGAGTCC CATCACAAGG 700

GTCATTTCAT CTACAAGAAT GTCTCAGAGG ACCTCCCCCT CCCCACCTTC 750

TCGCCCACAC TGCTGGGGGA CTCCCGCATG CTGTACTTCT GGTTCTCTGA 800

GCGAGTCTTC CACTCGCTGG CCAAGGTAGC TTTCCAGGAT GGCCGCCTCA 850

TGCTCAGCCT GATGGGAGAC GAGTTCAAGG CAGTGCTGGA GACCTGGGGC 900

TTCAACACCA ACCAGGAAAT CTTCCAAGAG GTTGTCGGCG GCTTCCCCAG 950

CCAGGCCCAA GTCACCGTCC ACTGCCTCAA GATGCCCAAG ATCTCCTGCC 1000

AAAACAAGGG AGTCGTGGTC AATTCTTCAG TGATGGTGAA ATTCCTCTTT 1050

CCACGCCCAG ACCAGCAACA TTCTGTAGCT TACACATTTG AAGAGGATAT 1100

CGTGACTACC GTCCAGGCCT CCTATTCTAA GAAAAAGCTC TTCTTAAGCC 1150

TCTTGGATTT CCAGATTACA CCAAAGACTG TTTCCAACTT GACTGAGAGC 1200

AGCTCCGAGT CCATCCAGAG CTTCCTGCAG TCAATGATCA CCGCTGTGGG 1250

CATCCCTGAG GTCATGTCTC GGCTCGAGGT AGTGTTTACA GCCCTCATGA 1300

ACAGCAAAGG CGTGAGCCTC TTCGACATCA TCAACCCTGA GATTATCACT 1350

CGAGATGGCT TCCTGCTGCT GCAGATGGAC TTTGGCTTCC CTGAGCACCT 1400

GCTGGTGGAT TTCCTCCAGA GCTTGAGC 1428

(2) INFORMATION FOR SEQ ID NO: 4:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 476 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (ix) FEATURE:
  - (A) NAME: Amino acid sequence of mature human CETP
  - (B) LOCATION:
- (x) PUBLICATION INFORMATION:
  - (A) AUTHORS: Drayna, Dennis, et al.
  - (B) TITLE: Cloning and sequencing of human cholesteryl ester transfer cDNA
  - (C) JOURNAL: Nature
  - (D) VOLUME: 327
  - (E) ISSUE:
  - (F) PAGES: 632 - 634
  - (G) DATE: 18-JUN-1987
  - (K) RELEVANT RESIDUES IN SEQ ID NO:4: FROM 1 TO 476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Cys Ser Lys Gly Thr Ser His Glu Ala Gly Ile Val Cys
1 5 10

Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn His Glu
15 20 25

Thr Ala Lys Val Ile Gln Thr Ala Phe Gln Arg Ala Ser

30 35

Tyr Pro Asp Ile Thr Gly Glu Lys Ala Met Met Leu Leu
40 45 50

Gly Gln Val Lys Tyr Gly Leu His Asn Ile Gln Ile Ser
55 60 65

His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Glu
70 75

Ala Lys Ser Ile Asp Val Ser Ile Gln Asn Val Ser Val
80 85 90

Val Phe Lys Gly Thr Leu Lys Tyr Gly Tyr Thr Thr Ala
95 100

Trp Trp Leu Gly Ile Asp Gln Ser Ile Asp Phe Glu Ile
105 110 115

Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Gln Leu Thr
120 125 130

Cys Asp Ser Gly Arg Val Arg Thr Asp Ala Pro Asp Cys
135 140

Tyr Leu Ser Phe His Lys Leu Leu Leu His Leu Gln Gly
145 150 155

Glu Arg Glu Pro Gly Trp Ile Lys Gln Leu Phe Thr Asn
160 165

Phe Ile Ser Phe Thr Leu Lys Leu Val Leu Lys Gly Gln
170 175 180

Ile Cys Lys Glu Ile Asn Val Ile Ser Asn Ile Met Ala
185 190 195

Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
200 205

Gly Asp Ile Gly Val Asp Ile Ser Leu Thr Gly Asp Pro
210 215 220

Val Ile Thr Ala Ser Tyr Leu Glu Ser His His Lys Gly
225 230

His Phe Ile Tyr Lys Asn Val Ser Glu Asp Leu Pro Leu
235 240 245

Pro Thr Phe Ser Pro Thr Leu Leu Gly Asp Ser Arg Met
250 255 260

Leu Tyr Phe Trp Phe Ser Glu Arg Val Phe His Ser Leu
265 270

Ala Lys Val Ala Phe Gln Asp Gly Arg Leu Met Leu Ser
275 280 285

Leu Met Gly Asp Glu Phe Lys Ala Val Leu Glu Thr Trp
290 295

Gly Phe Asn Thr Asn Gln Glu Ile Phe Gln Glu Val Val
300 305 310

Gly Gly Phe Pro Ser Gln Ala Gln Val Thr Val His Cys
315 320 325

Leu Lys Met Pro Lys Ile Ser Cys Gln Asn Lys Gly Val
330 335

Val Val Asn Ser Ser Val Met Val Lys Phe Leu Phe Pro
340 345 350

Arg Pro Asp Gln Gln His Ser Val Ala Tyr Thr Phe Glu
355 360

Glu Asp Ile Val Thr Thr Val Gln Ala Ser Tyr Ser Lys
365 370 375

Lys Lys Leu Phe Leu Ser Leu Leu Asp Phe Gln Ile Thr
380 385 390

Pro Lys Thr Val Ser Asn Leu Thr Glu Ser Ser Ser Glu
395 400

Ser Ile Gln Ser Phe Leu Gln Ser Met Ile Thr Ala Val
405 410 415

Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Val Phe
420 425

Thr Ala Leu Met Asn Ser Lys Gly Val Ser Leu Phe Asp
430 435 440

Ile Ile Asn Pro Glu Ile Ile Thr Arg Asp Gly Phe Leu
445 450 455

Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His Leu Leu
460 465

Val Asp Phe Leu Gln Ser Leu Ser
470 475

(2) INFORMATION FOR SEQ ID NO: 5:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE:
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE:

(A) NAME:
(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGGCCGCCA TGCAGTACAT CAAGGCCAAC TCCAAGTTCA TCGGCATCAC 50

GGAGCGCTTC CCCCGCCCAG ATGGCCGAGA AGCTGTGGCC TACAGGTTTG 100

AGGAGGATAT CTTCGGTTTT CCCAAGCACC TGCTGGTGGA TTTCCTGCAG 150

AGCCTGAGCT AGCGGCCGC 169

(2) INFORMATION FOR SEQ ID NO: 6:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE:
(A) NAME: Complementary strand to SEQ ID NO:5
(B) LOCATION: 1 to 169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCGGCCGCTA GCTCAGGCTC TGCAGGAAAT CCACCAGCAG GTGCTTGGGA 50

AAACCGAAGA TATCCTCCTC AAACCTGTAG GCCACAGCTT CTCGGCCATC 100

TGGGCGGGGG AAGCGCTCCG TGATGCCGAT GAACTTGGAG TTGGCCTTGA 150

TGTACTGCAT CGCGGCCGC 169

(2) INFORMATION FOR SEQ ID NO:7:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE: amino acid sequence of peptide encoded by bases 10 to 159 of SEQ ID NO:5
(A) NAME:
(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile
1 5 10

Thr Glu Arg Phe Pro Arg Pro Asp Gly Arg Glu Ala Val
15 20 25

Ala Tyr Arg Phe Glu Glu Asp Ile Phe Gly Phe Pro Lys
30 35

His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
40 45 50

(2) INFORMATION FOR SEQ ID NO:8:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1608 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE:
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE:
(A) NAME: translational stop codon
(B) LOCATION: 1606 - 1608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGCGCTGATG ATGTTGTTGA TTCTTCTAAA TCTTTTGTGA TGGAAAACTT 50

TTCTTCGTAC CACGGGACTA AACCTGGTTA TGTAGATTCC ATTCAAAAAG 100

GTATACAAAA GCCAAAATCT GGTACACAAG GAAATTATGA CGATGATTGG 150

AAAGGGTTTT ATAGTACCGA CAATAAATAC GACGCTGCGG GATACTCTGT 200

AGATAATGAA AACCCGCTCT CTGGAAAAGC TGGAGGCGTG GTCAAAGTGA 250

CGTATCCAGG ACTGACGAAG GTTCTCGCAC TAAAAGTGGA TAATGCCGAA 300

ACTATTAAGA AAGAGTTAGG TTTAAGTCTC ACTGAACCGT TGATGGAGCA 350

AGTCGGAACG GAAGAGTTTA TCAAAAGGTT CGGTGATGGT GCTTCGCGTG 400

TAGTGCTCAG CCTTCCCTTC GCTGAGGGGA GTTCTAGCGT TGAATATATT 450

AATAACTGGG AACAGGCGAA AGCGTTAAGC GTAGAACTTG AGATTAATTT 500

TGAAACCCGT GGAAAACGTG GCCAAGATGC GATGTATGAG TATATGGCTC 550

AAGCCTGTGC AGGAAATCGT GTCAGGCGAT CAGTAGGTAG CTCATTGTCA 600

TGCATAAATC TTGATTGGGA TGTCATAAGG GATAAAACTA AGACAAAGAT 650

AGAGTCTTTG AAAGAGCATG GCCCTATCAA AAATAAAATG AGCGAAAGTC 700

CCAATAAAAC AGTATCTGAG GAAAAAGCTA AACAATACCT AGAAGAATTT 750

CATCAAACGG CATTAGAGCA TCCTGAATTG TCAGAACTTA AAACCGTTAC 800

TGGGACCAAT CCTGTATTCG CTGGGGCTAA CTATGCGGCG TGGGCAGTAA 850

ACGTTGCGCA AGTTATCGAT AGCGAAACAG CTGATAATTT GGAAAAGACA 900

ACTGCTGCTC TTTCGATACT TCCTGGTATC GGTAGCGTAA TGGGCATTGC 950

AGACGGTGCC GTTCACCACA ATACAGAAGA GATAGTGGCA CAATCAATAG 1000

CTTTATCGTC TTTAATGGTT GCTCAAGCTA TTCCATTGGT AGGAGAGCTA 1050

GTTGATATTG GTTTCGCTGC ATATAATTTT GTAGAGAGTA TTATCAATTT 1100

ATTTCAAGTA GTTCATAATT CGTATAATCG TCCCGCGTAT TCTCCGGGGC 1150

ATAAAACGCA ACCATTTCTT CATGACGGGT ATGCTGTCAG TTGGAACACT 1200

GTTGAAGATT CGATAATCCG AACTGGTTTT CAAGGGGAGA GTGGGCACGA 1250

CATAAAAATT ACTGCTGAAA ATACCCCGCT TCCAATCGCG GGTGTCCTAC 1300

TACCGACTAT TCCTGGAAAG CTGGACGTTA ATAAGTCCAA GACTCATATT 1350

TCCGTAAATG GTCGGAAAAT AAGGATGCGT TGCAGAGCTA TAGACGGTGA 1400

TGTAACTTTT TGTCGCCCTA AATCTCCTGT TTATGTTGGT AATGGTGTGC 1450

ATGCGAATCT TCACGTGGCA TTTCACAGAA GCAGCTCGGA GAAAATTCAT 1500

TCTAATGAAA TTTCGTCGGA TTCCATAGGC GTTCTTGGGT ACCAGAAAAC 1550

AGTAGATCAC ACCAAGGTTA ATTCTAAGCT ATCGCTATTT TTTGAAATCA 1600

AAAGCTGA 1608

(2) INFORMATION FOR SEQ ID NO:9:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 535 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE:
(A) NAME:
(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met
1 5 10

Glu Asn Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val
15 20 25

Asp Ser Ile Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr
30 35 40

Gln Gly Asn Tyr Asp Asp Asp Trp Lys Gly Phe Tyr Ser Thr
45 50 55

Asp Asn Lys Tyr Asp Ala Ala Gly Tyr Ser Val Asp Asn Glu
60 65 70

Asn Pro Leu Ser Gly Lys Ala Gly Gly Val Val Lys Val Thr
75 80

Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val Asp Asn
85 90 95

Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu
100 105 110

Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg
115 120 125

Phe Gly Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe
130 135 140

Ala Glu Gly Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu
145 150

Gln Ala Lys Ala Leu Ser Val Glu Leu Glu Ile Asn Phe Glu
155 160 165

Thr Arg Gly Lys Arg Gly Gln Asp Ala Met Tyr Glu Tyr Met

170 175 180

Ala Gln Ala Cys Ala Gly Asn Arg Val Arg Arg Ser Val Gly
185 190 195

Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val Ile Arg
200 205 210

Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly
215 220

Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val
225 230 235

Ser Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln
240 245 250

Thr Ala Leu Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val
255 260 265

Thr Gly Thr Asn Pro Val Phe Ala Gly Ala Asn Tyr Ala Ala
270 275 280

Trp Ala Val Asn Val Ala Gln Val Ile Asp Ser Glu Thr Ala
285 290

Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu Ser Ile Leu Pro
295 300 305

Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala Val His
310 315 320

His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser
325 330 335

Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu
340 345 350

Val Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile
355 360

Ile Asn Leu Phe Gln Val Val His Asn Ser Tyr Asn Arg Pro
365 370 375

Ala Tyr Ser Pro Gly His Lys Thr Gln Pro Phe Leu His Asp
380 385 390

Gly Tyr Ala Val Ser Trp Asn Thr Val Glu Asp Ser Ile Ile
395 400 405

Arg Thr Gly Phe Gln Gly Glu Ser Gly His Asp Ile Lys Ile
410 415 420

Thr Ala Glu Asn Thr Pro Leu Pro Ile Ala Gly Val Leu Leu
425 430

Pro Thr Ile Pro Gly Lys Leu Asp Val Asn Lys Ser Lys Thr
435 440 445

```
His Ile Ser Val Asn Gly Arg Lys Ile Arg Met Arg Cys Arg
    450                 455                 460

Ala Ile Asp Gly Asp Val Thr Phe Cys Arg Pro Lys Ser Pro
        465                 470                 475

Val Tyr Val Gly Asn Gly Val His Ala Asn Leu His Val Ala
            480                 485                 490

Phe His Arg Ser Ser Ser Glu Lys Ile His Ser Asn Glu Ile
                495                 500

Ser Ser Asp Ser Ile Gly Val Leu Gly Tyr Gln Lys Thr Val
505                 510                 515

Asp His Thr Lys Val Asn Ser Lys Leu Ser Leu Phe Phe Glu
    520                 525                 530

Ile Lys Ser
        535
```

(2) INFORMATION FOR SEQ ID NO:10

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(ix) FEATURE:
- (A) NAME:
- (B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro
1               5                   10

Lys Val Ser Ala Ser His Leu Glu
    15                  20
```

SEQUENCE LISTING

(1) GENERAL INFORMATION:
(i) APPLICANT: Thomas, Lawrence J.

(ii) TITLE OF INVENTION: PLASMID-BASED VACCINE FOR TREATING ATHEROSCLEROSIS
(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Yankwich & Associates
(B) STREET: 130 Bishop Allen Drive
(C) CITY: Cambridge
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02139

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: Windows 95/98
(D) SOFTWARE: Word 97

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: (not yet assigned)
(B) FILING DATE: 30 April 2001
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION: 08/640,713
(B) FILING DATE: 01 May 1996 (01.05.96)

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION: 08/802,967
(B) FILING DATE: 21 February 1997 (21.02.97)

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION: 09/171,969
(B) FILING DATE: 29 October 1998 (29.10.98)

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Leon R. Yankwich
(B) REGISTRATION NUMBER: 30,237
(C) REFERENCE/DOCKET NUMBER: TCS-414.2 US-1

(2) INFORMATION FOR SEQ ID NO: 1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1488 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE: Structural coding sequence for

mature rabbit CETP
(A) NAME:
(B) LOCATION:
(x) PUBLICATION INFORMATION:
(A) AUTHORS: Nagashima, Mariko, et al.
(B) TITLE: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer protein
(C) JOURNAL: J. Lipid Res.
(D) VOLUME: 29
(E) ISSUE:
(F) PAGES: 1643 - 1649
(G) DATE: 1988
(K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 1488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TGTCCCAAAG GCGCCTCCTA CGAGGCTGGC ATCGTGTGTC GCATCACCAA 50

GCCCGCCCTC TTGGTGTTGA ACCAAGAGAC GGCCAAGGTG GTCCAGACGG 100

CCTTCCAGCG CGCCGGCTAT CCGGACGTCA GCGGCGAGAG GGCCGTGATG 150

CTCCTCGGCC GGGTCAAGTA CGGGCTGCAC AACCTCCAGA TCAGCCACCT 200

GTCCATCGCC AGCAGCCAGG TGGAGCTGGT GGACGCCAAG ACCATCGACG 250

TCGCCATCCA GAACGTGTCC GTGGTCTTCA AGGGGACCCT GAACTACAGC 300

TACACGAGTG CCTGGGGGTT GGGCATCAAT CAGTCTGTCG ACTTCGAGAT 350

CGACTCTGCC ATTGACCTCC AGATCAACAC AGAGCTGACC TGCGACGCTG 400

GCAGTGTGCG CACCAATGCC CCCGACTGCT ACCTGGCTTT CCATAAACTG 450

CTCCTGCACC TCCAGGGGGA GCGCGAGCCG GGGTGGCTCA AGCAGCTCTT 500

CACAAACTTC ATCTCCTTCA CCCTGAAGCT GATTCTGAAG CGACAGGTCT 550

GCAATGAGAT CAACACCATC TCCAACATCA TGGCTGACTT TGTCCAGACG 600

AGGGCCGCCA GCATCCTCTC AGATGGAGAC ATCGGGGTGG ACATTTCCGT 650

GACGGGGGCC CCTGTCATCA CAGCCACCTA CCTGGAGTCC CATCACAAGG 700

GTCACTTCAC GCACAAGAAC GTCTCCGAGG CCTTCCCCCT CCGCGCCTTC 750

CCGCCCGGTC TTCTGGGGGA CTCCCGCATG CTCTACTTCT GGTTCTCCGA 800

TCAAGTGCTC AACTCCCTGG CCAGGGCCGC CTTCCAGGAG GGCCGTCTCG 850

TGCTCAGCCT GACAGGGGAT GAGTTCAAGA AAGTGCTGGA GACCCAGGGT 900

TTCGACACCA ACCAGGAAAT CTTCCAGGAG CTTTCCAGAG GCCTTCCCAC 950

CGGCCAGGCC CAGGTAGCCG TCCACTGCCT TAAGGTGCCC AAGATCTCCT 1000

GCCAGAACCG GGGTGTCGTG GTGTCTTCTT CCGTCGCCGT GACGTTCCGC 1050

TTCCCCCGCC CAGATGGCCG AGAAGCTGTG GCCTACAGGT TTGAGGAGGA 1100

TATCATCACC ACCGTCCAGG CCTCCTACTC CCAGAAAAAG CTCTTCCTAC 1150

ACCTCTTGGA TTTCCAGTGC GTGCCGGCCA GCGGAAGGGC AGGCAGCTCA 1200

GCAAATCTCT CCGTGGCCCT CAGGACTGAG GCTAAGGCTG TTTCCAACCT 1250

GACTGAGAGC CGCTCCGAGT CCCTGCAGAG CTCTCTCCGC TCCCTGATCG 1300

CCACGGTGGG CATCCCGGAG GTCATGTCTC GGCTCGAGGT GGCGTTCACA 1350

GCCCTCATGA ACAGCAAAGG CCTGGACCTC TTCGAAATCA TCAACCCCGA 1400

GATTATCACT CTCGATGGCT GCCTGCTGCT GCAGATGGAC TTCGGTTTTC 1450

CCAAGCACCT GCTGGTGGAT TTCCTGCAGA GCCTGAGC 1488

(2) INFORMATION FOR SEQ ID NO:2:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 496 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE:
(A) NAME: Amino acid sequence for mature rabbit CETP protein.
(B) LOCATION:

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Nagashima, Mariko, et al.
(B) TITLE: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer protein
(C) JOURNAL: J. Lipid Res.
(D) VOLUME: 29
(E) ISSUE:
(F) PAGES: 1643 - 1649
(G) DATE: 1988
(K) RELEVANT RESIDUES IN SEQ ID NO:2: FROM 1 TO 496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Cys Pro Lys Gly Ala Ser Tyr Glu Ala Gly Ile Val Cys
1 5 10

Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn Gln Glu
15 20 25

Thr Ala Lys Val Val Gln Thr Ala Phe Gln Arg Ala Gly
30 35

Tyr Pro Asp Val Ser Gly Glu Arg Ala Val Met Leu Leu
40 45 50

Gly Arg Val Lys Tyr Gly Leu His Asn Leu Gln Ile Ser
55 60 65

His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Asp
70 75

Ala Lys Thr Ile Asp Val Ala Ile Gln Asn Val Ser Val
80 85 90

Val Phe Lys Gly Thr Leu Asn Tyr Ser Tyr Thr Ser Ala
95 100

Trp Gly Leu Gly Ile Asn Gln Ser Val Asp Phe Glu Ile
105 110 115

Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Glu Leu Thr
120 125 130

Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp Cys
135 140

Tyr Leu Ala Phe His Lys Leu Leu Leu His Leu Gln Gly
145 150 155

Glu Arg Glu Pro Gly Trp Leu Lys Gln Leu Phe Thr Asn
160 165

Phe Ile Ser Phe Thr Leu Lys Leu Ile Leu Lys Arg Gln
170 175 180

Val Cys Asn Glu Ile Asn Thr Ile Ser Asn Ile Met Ala
185 190 195

Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
200 205

Gly Asp Ile Gly Val Asp Ile Ser Val Thr Gly Ala Pro
210 215 220

Val Ile Thr Ala Thr Tyr Leu Glu Ser His His Lys Gly
225 230

His Phe Thr His Lys Asn Val Ser Glu Ala Phe Pro Leu
235 240 245

Arg Ala Phe Pro Pro Gly Leu Leu Gly Asp Ser Arg Met
250 255 260

Leu Tyr Phe Trp Phe Ser Asp Gln Val Leu Asn Ser Leu

265 270

Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser
275 280 285

Leu Thr Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln
290 295

Gly Phe Asp Thr Asn Gln Glu Ile Phe Gln Glu Leu Ser
300 305 310

Arg Gly Leu Pro Thr Gly Gln Ala Gln Val Ala Val His
315 320 325

Cys Leu Lys Val Pro Lys Ile Ser Cys Gln Asn Arg Gly
330 335

Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe
340 345 350

Pro Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe
355 360

Glu Glu Asp Ile Ile Thr Thr Val Gln Ala Ser Tyr Ser
365 370 375

Gln Lys Lys Leu Phe Leu His Leu Leu Asp Phe Gln Cys
380 385 390

Val Pro Ala Ser Gly Arg Ala Gly Ser Ser Ala Asn Leu
395 400

Ser Val Ala Leu Arg Thr Glu Ala Lys Ala Val Ser Asn
405 410 415

Leu Thr Glu Ser Arg Ser Glu Ser Leu Gln Ser Ser Leu
420 425

Arg Ser Leu Ile Ala Thr Val Gly Ile Pro Glu Val Met
430 435 440

Ser Arg Leu Glu Val Ala Phe Thr Ala Leu Met Asn Ser
445 450 455

Lys Gly Leu Asp Leu Phe Glu Ile Ile Asn Pro Glu Ile
460 465

Ile Thr Leu Asp Gly Cys Leu Leu Leu Gln Met Asp Phe
470 475 480

Gly Phe Pro Lys His Leu Leu Val Asp Phe Leu Gln Ser
485 490

Leu Ser
495

(2) INFORMATION FOR SEQ ID NO: 3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1428 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE:
(A) NAME: Structural coding sequence for mature human CETP
(B) LOCATION:
(x) PUBLICATION INFORMATION:
(A) AUTHORS: Drayna, Dennis, et al.
(B) TITLE: Cloning and sequencing of human cholesteryl ester transfer cDNA
(C) JOURNAL: Nature
(D) VOLUME: 327
(E) ISSUE:
(F) PAGES: 632 - 634
(G) DATE: 18-JUN-1987
(K) RELEVANT RESIDUES IN SEQ ID NO:3: FROM 1 TO 1428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGCTCCAAAG GCACCTCGCA CGAGGCAGGC ATCGTGTGCC GCATCACCAA 50

GCCTGCCCTC CTGGTGTTGA ACCACGAGAC TGCCAAGGTG ATCCAGACCG 100

CCTTCCAGCG AGCCAGCTAC CCAGATATCA CGGGCGAGAA GGCCATGATG 150

CTCCTTGGCC AAGTCAAGTA TGGGTTGCAC AACATCCAGA TCAGCCACTT 200

GTCCATCGCC AGCAGCCAGG TGGAGCTGGT GGAAGCCAAG TCCATTGATG 250

TCTCCATTCA GAACGTGTCT GTGGTCTTCA AGGGGACCCT GAAGTATGGC 300

TACACCACTG CCTGGTGGCT GGGTATTGAT CAGTCCATTG ACTTCGAGAT 350

CGACTCTGCC ATTGACCTCC AGATCAACAC ACAGCTGACC TGTGACTCTG 400

GTAGAGTGCG GACCGATGCC CCTGACTGCT ACCTGTCTTT CCATAAGCTG 450

CTCCTGCATC TCCAAGGGGA GCGAGAGCCT GGGTGGATCA AGCAGCTGTT 500

CACAAATTTC ATCTCCTTCA CCCTGAAGCT GGTCCTGAAG GGACAGATCT 550

GCAAAGAGAT CAACGTCATC TCTAACATCA TGGCCGATTT TGTCCAGACA 600

AGGGCTGCCA GCATCCTTTC AGATGGAGAC ATTGGGGTGG ACATTTCCCT 650

GACAGGTGAT CCCGTCATCA CAGCCTCCTA CCTGGAGTCC CATCACAAGG 700

GTCATTTCAT CTACAAGAAT GTCTCAGAGG ACCTCCCCCT CCCCACCTTC 750

TCGCCCACAC TGCTGGGGGA CTCCCGCATG CTGTACTTCT GGTTCTCTGA 800

GCGAGTCTTC CACTCGCTGG CCAAGGTAGC TTTCCAGGAT GGCCGCCTCA 850

TGCTCAGCCT GATGGGAGAC GAGTTCAAGG CAGTGCTGGA GACCTGGGGC 900

TTCAACACCA ACCAGGAAAT CTTCCAAGAG GTTGTCGGCG GCTTCCCCAG 950

CCAGGCCCAA GTCACCGTCC ACTGCCTCAA GATGCCCAAG ATCTCCTGCC 1000

AAAACAAGGG AGTCGTGGTC AATTCTTCAG TGATGGTGAA ATTCCTCTTT 1050

CCACGCCCAG ACCAGCAACA TTCTGTAGCT TACACATTTG AAGAGGATAT 1100

CGTGACTACC GTCCAGGCCT CCTATTCTAA GAAAAAGCTC TTCTTAAGCC 1150

TCTTGGATTT CCAGATTACA CCAAAGACTG TTTCCAACTT GACTGAGAGC 1200

AGCTCCGAGT CCATCCAGAG CTTCCTGCAG TCAATGATCA CCGCTGTGGG 1250

CATCCCTGAG GTCATGTCTC GGCTCGAGGT AGTGTTTACA GCCCTCATGA 1300

ACAGCAAAGG CGTGAGCCTC TTCGACATCA TCAACCCTGA GATTATCACT 1350

CGAGATGGCT TCCTGCTGCT GCAGATGGAC TTTGGCTTCC CTGAGCACCT 1400

GCTGGTGGAT TTCCTCCAGA GCTTGAGC 1428

(2) INFORMATION FOR SEQ ID NO: 4:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 476 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE:
(A) NAME: Amino acid sequence of mature human CETP
(B) LOCATION:
(x) PUBLICATION INFORMATION:
(A) AUTHORS: Drayna, Dennis, et al.
(B) TITLE: Cloning and sequencing of human cholesteryl ester transfer cDNA
(C) JOURNAL: Nature
(D) VOLUME: 327
(E) ISSUE:
(F) PAGES: 632 - 634
(G) DATE: 18-JUN-1987
(K) RELEVANT RESIDUES IN SEQ ID NO:4: FROM 1 TO 476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Cys Ser Lys Gly Thr Ser His Glu Ala Gly Ile Val Cys
1 5 10

Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn His Glu
15 20 25

Thr Ala Lys Val Ile Gln Thr Ala Phe Gln Arg Ala Ser
30 35

Tyr Pro Asp Ile Thr Gly Glu Lys Ala Met Met Leu Leu
40 45 50

Gly Gln Val Lys Tyr Gly Leu His Asn Ile Gln Ile Ser
55 60 65

His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Glu
70 75

Ala Lys Ser Ile Asp Val Ser Ile Gln Asn Val Ser Val
80 85 90

Val Phe Lys Gly Thr Leu Lys Tyr Gly Tyr Thr Thr Ala
95 100

Trp Trp Leu Gly Ile Asp Gln Ser Ile Asp Phe Glu Ile
105 110 115

Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Gln Leu Thr
120 125 130

Cys Asp Ser Gly Arg Val Arg Thr Asp Ala Pro Asp Cys
135 140

Tyr Leu Ser Phe His Lys Leu Leu Leu His Leu Gln Gly
145 150 155

Glu Arg Glu Pro Gly Trp Ile Lys Gln Leu Phe Thr Asn
160 165

Phe Ile Ser Phe Thr Leu Lys Leu Val Leu Lys Gly Gln
170 175 180

Ile Cys Lys Glu Ile Asn Val Ile Ser Asn Ile Met Ala
185 190 195

Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
200 205

Gly Asp Ile Gly Val Asp Ile Ser Leu Thr Gly Asp Pro
210 215 220

Val Ile Thr Ala Ser Tyr Leu Glu Ser His His Lys Gly
225 230

His Phe Ile Tyr Lys Asn Val Ser Glu Asp Leu Pro Leu
235 240 245

Pro Thr Phe Ser Pro Thr Leu Leu Gly Asp Ser Arg Met
250 255 260

Leu Tyr Phe Trp Phe Ser Glu Arg Val Phe His Ser Leu
265 270

Ala Lys Val Ala Phe Gln Asp Gly Arg Leu Met Leu Ser
275 280 285

Leu Met Gly Asp Glu Phe Lys Ala Val Leu Glu Thr Trp
290 295

Gly Phe Asn Thr Asn Gln Glu Ile Phe Gln Glu Val Val
300 305 310

Gly Gly Phe Pro Ser Gln Ala Gln Val Thr Val His Cys
315 320 325

Leu Lys Met Pro Lys Ile Ser Cys Gln Asn Lys Gly Val
330 335

Val Val Asn Ser Ser Val Met Val Lys Phe Leu Phe Pro
340 345 350

Arg Pro Asp Gln Gln His Ser Val Ala Tyr Thr Phe Glu
355 360

Glu Asp Ile Val Thr Thr Val Gln Ala Ser Tyr Ser Lys
365 370 375

Lys Lys Leu Phe Leu Ser Leu Leu Asp Phe Gln Ile Thr
380 385 390

Pro Lys Thr Val Ser Asn Leu Thr Glu Ser Ser Ser Glu
395 400

Ser Ile Gln Ser Phe Leu Gln Ser Met Ile Thr Ala Val
405 410 415

Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Val Phe
420 425

Thr Ala Leu Met Asn Ser Lys Gly Val Ser Leu Phe Asp
430 435 440

Ile Ile Asn Pro Glu Ile Ile Thr Arg Asp Gly Phe Leu
445 450 455

Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His Leu Leu
460 465

Val Asp Phe Leu Gln Ser Leu Ser
470 475

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE:
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE:
(A) NAME:
(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGGCCGCCA TGCAGTACAT CAAGGCCAAC TCCAAGTTCA TCGGCATCAC 50

GGAGCGCTTC CCCCGCCCAG ATGGCCGAGA AGCTGTGGCC TACAGGTTTG 100

AGGAGGATAT CTTCGGTTTT CCCAAGCACC TGCTGGTGGA TTTCCTGCAG 150

AGCCTGAGCT AGCGGCCGC 169

(2) INFORMATION FOR SEQ ID NO: 6:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE:
(A) NAME: Complementary strand to SEQ ID NO:5
(B) LOCATION: 1 to 169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCGGCCGCTA GCTCAGGCTC TGCAGGAAAT CCACCAGCAG GTGCTTGGGA 50

AAACCGAAGA TATCCTCCTC AAACCTGTAG GCCACAGCTT CTCGGCCATC 100

TGGGCGGGGG AAGCGCTCCG TGATGCCGAT GAACTTGGAG TTGGCCTTGA 150

TGTACTGCAT CGCGGCCGC 169

(2) INFORMATION FOR SEQ ID NO:7:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE: amino acid sequence of peptide encoded by bases 10 to 159 of SEQ ID NO:5

(A) NAME:
(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile
1               5                   10

Thr Glu Arg Phe Pro Arg Pro Asp Gly Arg Glu Ala Val
    15                  20                  25

Ala Tyr Arg Phe Glu Glu Asp Ile Phe Gly Phe Pro Lys
            30                  35

His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
40                  45                  50
```

(2) INFORMATION FOR SEQ ID NO:8:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1608 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE:
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE:
(A) NAME: translational stop codon
(B) LOCATION: 1606 - 1608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
GGCGCTGATG ATGTTGTTGA TTCTTCTAAA TCTTTTGTGA TGGAAAACTT     50

TTCTTCGTAC CACGGGACTA AACCTGGTTA TGTAGATTCC ATTCAAAAAG    100

GTATACAAAA GCCAAAATCT GGTACACAAG GAAATTATGA CGATGATTGG    150

AAAGGGTTTT ATAGTACCGA CAATAAATAC GACGCTGCGG GATACTCTGT    200

AGATAATGAA AACCCGCTCT CTGGAAAAGC TGGAGGCGTG GTCAAAGTGA    250

CGTATCCAGG ACTGACGAAG GTTCTCGCAC TAAAAGTGGA TAATGCCGAA    300

ACTATTAAGA AAGAGTTAGG TTTAAGTCTC ACTGAACCGT TGATGGAGCA    350

AGTCGGAACG GAAGAGTTTA TCAAAAGGTT CGGTGATGGT GCTTCGCGTG    400

TAGTGCTCAG CCTTCCCTTC GCTGAGGGGA GTTCTAGCGT TGAATATATT    450

AATAACTGGG AACAGGCGAA AGCGTTAAGC GTAGAACTTG AGATTAATTT    500

TGAAACCCGT GGAAAACGTG GCCAAGATGC GATGTATGAG TATATGGCTC    550

AAGCCTGTGC AGGAAATCGT GTCAGGCGAT CAGTAGGTAG CTCATTGTCA    600
```

TGCATAAATC TTGATTGGGA TGTCATAAGG GATAAAACTA AGACAAAGAT 650

AGAGTCTTTG AAAGAGCATG GCCCTATCAA AAATAAAATG AGCGAAAGTC 700

CCAATAAAAC AGTATCTGAG GAAAAAGCTA AACAATACCT AGAAGAATTT 750

CATCAAACGG CATTAGAGCA TCCTGAATTG TCAGAACTTA AAACCGTTAC 800

TGGGACCAAT CCTGTATTCG CTGGGGCTAA CTATGCGGCG TGGGCAGTAA 850

ACGTTGCGCA AGTTATCGAT AGCGAAACAG CTGATAATTT GGAAAAGACA 900

ACTGCTGCTC TTTCGATACT TCCTGGTATC GGTAGCGTAA TGGGCATTGC 950

AGACGGTGCC GTTCACCACA ATACAGAAGA GATAGTGGCA CAATCAATAG 1000

CTTTATCGTC TTTAATGGTT GCTCAAGCTA TTCCATTGGT AGGAGAGCTA 1050

GTTGATATTG GTTTCGCTGC ATATAATTTT GTAGAGAGTA TTATCAATTT 1100

ATTTCAAGTA GTTCATAATT CGTATAATCG TCCCGCGTAT TCTCCGGGGC 1150

ATAAAACGCA ACCATTTCTT CATGACGGGT ATGCTGTCAG TTGGAACACT 1200

GTTGAAGATT CGATAATCCG AACTGGTTTT CAAGGGGAGA GTGGGCACGA 1250

CATAAAAATT ACTGCTGAAA ATACCCCGCT TCCAATCGCG GGTGTCCTAC 1300

TACCGACTAT TCCTGGAAAG CTGGACGTTA ATAAGTCCAA GACTCATATT 1350

TCCGTAAATG GTCGGAAAAT AAGGATGCGT TGCAGAGCTA TAGACGGTGA 1400

TGTAACTTTT TGTCGCCCTA AATCTCCTGT TTATGTTGGT AATGGTGTGC 1450

ATGCGAATCT TCACGTGGCA TTTCACAGAA GCAGCTCGGA GAAAATTCAT 1500

TCTAATGAAA TTTCGTCGGA TTCCATAGGC GTTCTTGGGT ACCAGAAAAC 1550

AGTAGATCAC ACCAAGGTTA ATTCTAAGCT ATCGCTATTT TTTGAAATCA 1600

AAAGCTGA 1608

(2) INFORMATION FOR SEQ ID NO:9:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 535 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE: (A) NAME:
(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met
1 5 10

Glu Asn Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val
15 20 25

Asp Ser Ile Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr
30 35 40

Gln Gly Asn Tyr Asp Asp Asp Trp Lys Gly Phe Tyr Ser Thr
45 50 55

Asp Asn Lys Tyr Asp Ala Ala Gly Tyr Ser Val Asp Asn Glu
60 65 70

Asn Pro Leu Ser Gly Lys Ala Gly Gly Val Val Lys Val Thr
75 80

Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val Asp Asn
85 90 95

Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu
100 105 110

Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg
115 120 125

Phe Gly Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe
130 135 140

Ala Glu Gly Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu
145 150

Gln Ala Lys Ala Leu Ser Val Glu Leu Glu Ile Asn Phe Glu
155 160 165

Thr Arg Gly Lys Arg Gly Gln Asp Ala Met Tyr Glu Tyr Met
170 175 180

Ala Gln Ala Cys Ala Gly Asn Arg Val Arg Arg Ser Val Gly
185 190 195

Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val Ile Arg
200 205 210

Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly
215 220

Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val
225 230 235

Ser Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln
240 245 250

Thr Ala Leu Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val
255 260 265

Thr Gly Thr Asn Pro Val Phe Ala Gly Ala Asn Tyr Ala Ala
270 275 280

Trp Ala Val Asn Val Ala Gln Val Ile Asp Ser Glu Thr Ala
285 290

Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu Ser Ile Leu Pro
295 300 305

Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala Val His
310 315 320

His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser
325 330 335

Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu
340 345 350

Val Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile
355 360

Ile Asn Leu Phe Gln Val Val His Asn Ser Tyr Asn Arg Pro
365 370 375

Ala Tyr Ser Pro Gly His Lys Thr Gln Pro Phe Leu His Asp
380 385 390

Gly Tyr Ala Val Ser Trp Asn Thr Val Glu Asp Ser Ile Ile
395 400 405

Arg Thr Gly Phe Gln Gly Glu Ser Gly His Asp Ile Lys Ile
410 415 420

Thr Ala Glu Asn Thr Pro Leu Pro Ile Ala Gly Val Leu Leu
425 430

Pro Thr Ile Pro Gly Lys Leu Asp Val Asn Lys Ser Lys Thr
435 440 445

His Ile Ser Val Asn Gly Arg Lys Ile Arg Met Arg Cys Arg
450 455 460

Ala Ile Asp Gly Asp Val Thr Phe Cys Arg Pro Lys Ser Pro
465 470 475

Val Tyr Val Gly Asn Gly Val His Ala Asn Leu His Val Ala
480 485 490

Phe His Arg Ser Ser Ser Glu Lys Ile His Ser Asn Glu Ile
495 500

Ser Ser Asp Ser Ile Gly Val Leu Gly Tyr Gln Lys Thr Val
505 510 515

Asp His Thr Lys Val Asn Ser Lys Leu Ser Leu Phe Phe Glu
520 525 530

Ile Lys Ser
535

(2) INFORMATION FOR SEQ ID NO:10
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE:
(A) NAME:
(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro
1 5 10

Lys Val Ser Ala Ser His Leu Glu
15 20

SEQUENCE LISTING

(1) GENERAL INFORMATION:
(i) APPLICANT: Thomas, Lawrence J.

(ii) TITLE OF INVENTION: PLASMID-BASED VACCINE FOR TREATING ATHEROSCLEROSIS

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Banner & Witcoff, Ltd.
(B) STREET: 75 State Street, Suite 2300
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02109-1807

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WordPerfect 6.1

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: (not yet assigned)
(B) FILING DATE: 01 May 1997 (01.05.97)
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION: 08/640,713
(B) FILING DATE: 01 May 1996 (01.05.96)

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION: 08/802,967
(B) FILING DATE: 21 February 1997 (21.02.97)

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Leon R. Yankwich
(B) REGISTRATION NUMBER: 30,237
(C) REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)

(2) INFORMATION FOR SEQ ID NO: 1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1488 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE: Structural coding sequence for mature rabbit CETP
(A) NAME:
(B) LOCATION:
(x) PUBLICATION INFORMATION:
(A) AUTHORS: Nagashima, Mariko, et al.

(B) TITLE: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer protein
(C) JOURNAL: J. Lipid Res.
(D) VOLUME: 29
(E) ISSUE:
(F) PAGES: 1643 - 1649
(G) DATE: 1988
(K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 1488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TGTCCCAAAG GCGCCTCCTA CGAGGCTGGC ATCGTGTGTC GCATCACCAA 50

GCCCGCCCTC TTGGTGTTGA ACCAAGAGAC GGCCAAGGTG GTCCAGACGG 100

CCTTCCAGCG CGCCGGCTAT CCGGACGTCA GCGGCGAGAG GGCCGTGATG 150

CTCCTCGGCC GGGTCAAGTA CGGGCTGCAC AACCTCCAGA TCAGCCACCT 200

GTCCATCGCC AGCAGCCAGG TGGAGCTGGT GGACGCCAAG ACCATCGACG 250

TCGCCATCCA GAACGTGTCC GTGGTCTTCA AGGGGACCCT GAACTACAGC 300

TACACGAGTG CCTGGGGGTT GGGCATCAAT CAGTCTGTCG ACTTCGAGAT 350

CGACTCTGCC ATTGACCTCC AGATCAACAC AGAGCTGACC TGCGACGCTG 400

GCAGTGTGCG CACCAATGCC CCCGACTGCT ACCTGGCTTT CCATAAACTG 450

CTCCTGCACC TCCAGGGGGA GCGCGAGCCG GGGTGGCTCA AGCAGCTCTT 500

CACAAACTTC ATCTCCTTCA CCCTGAAGCT GATTCTGAAG CGACAGGTCT 550

GCAATGAGAT CAACACCATC TCCAACATCA TGGCTGACTT TGTCCAGACG 600

AGGGCCGCCA GCATCCTCTC AGATGGAGAC ATCGGGGTGG ACATTTCCGT 650

GACGGGGGCC CCTGTCATCA CAGCCACCTA CCTGGAGTCC CATCACAAGG 700

GTCACTTCAC GCACAAGAAC GTCTCCGAGG CCTTCCCCCT CCGCGCCTTC 750

CCGCCCGGTC TTCTGGGGGA CTCCCGCATG CTCTACTTCT GGTTCTCCGA 800

TCAAGTGCTC AACTCCCTGG CCAGGGCCGC CTTCCAGGAG GGCCGTCTCG 850

TGCTCAGCCT GACAGGGGAT GAGTTCAAGA AAGTGCTGGA GACCCAGGGT 900

TTCGACACCA ACCAGGAAAT CTTCCAGGAG CTTTCCAGAG GCCTTCCCAC 950

CGGCCAGGCC CAGGTAGCCG TCCACTGCCT TAAGGTGCCC AAGATCTCCT 1000

GCCAGAACCG GGGTGTCGTG GTGTCTTCTT CCGTCGCCGT GACGTTCCGC 1050

TTCCCCCGCC CAGATGGCCG AGAAGCTGTG GCCTACAGGT TTGAGGAGGA 1100

TATCATCACC ACCGTCCAGG CCTCCTACTC CCAGAAAAAG CTCTTCCTAC 1150

ACCTCTTGGA TTTCCAGTGC GTGCCGGCCA GCGGAAGGGC AGGCAGCTCA 1200

GCAAATCTCT CCGTGGCCCT CAGGACTGAG GCTAAGGCTG TTTCCAACCT 1250

GACTGAGAGC CGCTCCGAGT CCCTGCAGAG CTCTCTCCGC TCCCTGATCG 1300

CCACGGTGGG CATCCCGGAG GTCATGTCTC GGCTCGAGGT GGCGTTCACA 1350

GCCCTCATGA ACAGCAAAGG CCTGGACCTC TTCGAAATCA TCAACCCCGA 1400

GATTATCACT CTCGATGGCT GCCTGCTGCT GCAGATGGAC TTCGGTTTTC 1450

CCAAGCACCT GCTGGTGGAT TTCCTGCAGA GCCTGAGC 1488

(2) INFORMATION FOR SEQ ID NO:2:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 496 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE:
(A) NAME: Amino acid sequence for mature rabbit CETP protein.
(B) LOCATION:

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Nagashima, Mariko, et al.
(B) TITLE: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer protein
(C) JOURNAL: J. Lipid Res.
(D) VOLUME: 29
(E) ISSUE:
(F) PAGES: 1643 - 1649
(G) DATE: 1988
(K) RELEVANT RESIDUES IN SEQ ID NO:2: FROM 1 TO 496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Cys Pro Lys Gly Ala Ser Tyr Glu Ala Gly Ile Val Cys
1 5 10

Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn Gln Glu
15 20 25

Thr Ala Lys Val Val Gln Thr Ala Phe Gln Arg Ala Gly
30 35

Tyr Pro Asp Val Ser Gly Glu Arg Ala Val Met Leu Leu